



**Exhibit A**  
**C mparison SEQ ID NO:4 vs. IPI00044749.2**

FASTA searches a protein or DNA sequence data bank  
version 3.3t05 March 30, 2000

Please cite:

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

```
/tmp.fastaCAAxJayWj: 1214 aa
>seqid4
vs /tmp.fastaDAAyJayWj library
searching /tmp.fastaDAAyJayWj library
```

1258 residues in 1 sequences

FASTA (3.34 January 2000) function [optimized; BL50 matrix (15:-5)] ktup: 2  
join: 40, opt: 28, gap-pen: -12/ -2, width: 16  
Scan time: 0.066  
The best scores are: opt  
IPI00044749.2 (1258) 4775

>>**IPI00044749.2**

(1258 aa)

initn: 4773 init1: 4773 opt: 4775  
Smith-Waterman score: 7822; 96.343% identity in 1258 aa overlap (1-1214:1-1258)

|   |        |        |        |        |        |
|---|--------|--------|--------|--------|--------|
| 10  | 20     | 30     | 40     | 50     | 60     |
| seqid4 MEKYVRLQKIGEGSGFGKAILVKSTEDGRQYVIKEINISRMSSKEREESRREAVLANMKH   | :::::: | :::::: | :::::: | :::::: | :::::: |
| IPI000 MEKYVRLQKIGEGSGFGKAILVKSTEDGRQYVIKEINISRMSSKEREESRREAVLANMKH   | 10     | 20     | 30     | 40     | 50     |
| 70  | 80     | 90     | 100    | 110    | 120    |
| seqid4 PNIVQYRESFEENGSLYIVMDYCEGGDLFKRINAQKGVLFQEDQILDWFVQICLALKHVH   | :::::: | :::::: | :::::: | :::::: | :::::: |
| IPI000 PNIVQYRESFEENGSLYIVMDYCEGGDLFKRINAQKGVLFQEDQILDWFVQICLALKHVH   | 70     | 80     | 90     | 100    | 110    |
| 130   | 140    | 150    | 160    | 170    | 180    |
| seqid4 DRKILHRDIKSQNIFLTKDGTVQLGDFGIARVLNSTVELARTCIGTPYYLSPEICENKPY   | :::::: | :::::: | :::::: | :::::: | :::::: |
| IPI000 DRKILHRDIKSQNIFLTKDGTVQLGDFGIARVLNSTVELARTCIGTPYYLSPEICENKPY   | 130    | 140    | 150    | 160    | 170    |
| 190   | 200    | 210    | 220    | 230    | 240    |
| seqid4 NNKSDI WALGCVLYELCTLKHAFEAGSMKNLVLKIISGSFPPVSLHYSYDLRSLVSQLFK  | :::::: | :::::: | :::::: | :::::: | :::::: |
| IPI000 NNKSDI WALGCVLYELCTLKHAFEAGSMKNLVLKIISGSFPPVSLHYSYDLRSLVSQLFK  | 190    | 200    | 210    | 220    | 230    |
| 250   | 260    | 270    | 280    | 290    | 300    |
| seqid4 RNPRDRPSVNSILEKGFIAKRIEKFLSPQLIAEEFCLKTFSKFGSQPIPAPKRPA\$GQNSI | :::::: | :::::: | :::::: | :::::: | :::::: |
| IPI000 RNPRDRPSVNSILEKGFIAKRIEKFLSPQLIAEEFCLKTFSKFGSQPIPAPKRPA\$GQNSI | 250    | 260    | 270    | 280    | 290    |
| 310   | 320    | 330    | 340    | 350    | 360    |
| seqid4 SVMPAQKITKPAAKYGIPLAYKKYGDKKLHEKKPLQHKHQAHQTPEKRVNTGEERRKISE   | :::::: | :::::: | :::::: | :::::: | :::::: |

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::::::: IPI000 SVMPAQKITKPAAKYGIPLAYKKYGDKKLHEKKPLQKHQAHTPEKRVNTGEERRKISE
      310      320      330      340      350      360
      370      380      390      400      410      420
seqid4 EAARKRRLEFIEKEKKQKDQIISLMKAEQMKRQEKERLERINRAREQGWRNVLSAGGSGE
::::::: IPI000 EAARKRRLEFIEKEKKQKDQIISLMKAEQMKRQEKERLERINRAREQGWRNVLSAGGSGE
      370      380      390      400      410      420
      430      440      450      460      470
seqid4 VKAPFLGSGGTIAPSSFSSRGQYEHYHAIFDQMQQRAEDNEAKWKREIYGRGLPER---
::::::: IPI000 VKAPFLGSGGTIAPSSFSSRGQYEHYHAIFDQMQQRAEDNEAKWKREIYGRGLPERGIL
      430      440      450      460      470      480
      490      500      510      520      530      540      550
seqid4 KREAMQNKARAEGHMHVYLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM
::::::: IPI000 KREAMQNKARAEGHMHVYLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM
      550      560      570      580      590      600      610
seqid4 RRKKIESLKAHANARAAVLKEQLERKRKEAYEREKKVWEELVAKGVKSSDVSPPLGQHE
::::::: IPI000 RRKKIESLKAHANARAAVLKEQLERKRKEAYEREKKVWEELVAKGVKSSDVSPPLGQHE
      610      620      630      640      650      660      670
seqid4 TGGSPSKQQMRSVISVTSALEKEVGVDSSLTDRETSEEMQTKTNAISSKREILRRLNENL
::::::: IPI000 TGGSPSKQQMRSVISVTSALEKEVGVDSSLTDRETSEEMQTKTNAISSKREILRRLNENL
      670      680      690      700      710      720
      680      690      700      710      720      730
seqid4 KAQEDEKGKQNLSDTFFEINVHEDAKEHEKEKEKSVDKWEAGGQLVIPLDETLDTFS
::::::: IPI000 KAQEDEKGKQNLSDTFFEINVHEDAKEHEKEKEKSVDKWEAGGQLVIPLDETLDTFS
      730      740      750      760      770      780      790
seqid4 TTERHTVGEVIKLGPNGSPPRAWGKSPTDSDLKILGEAELQLQTELLENTTIRSEISPEG
::::::: IPI000 TTERHTVGEVIKLGPNGSPPRAWGKSPTDSDLKILGEAELQLQTELLENTTIRSEISPEG
      790      800      810      820      830      840
      800      810      820      830      840      850
seqid4 EKYKPLITGEKKVQCISHEINPSAIVDSPVETKSPEFSEASQPMSLKLEGNLEEPDDLET
::::::: IPI000 EKYKPLITGEKKVQCISHEINPSAIVDSPVETKSPEFSEASQPMSLKLEGNLEEPDDLET
      850      860      870      880      890      900      910
seqid4 EILQEPSTGNKDESLPCTITDWISEEKETKETQSADRITIQENEVSEGDVSSTVDQLSD
:::::::

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IPI000 EILQEPSTNKDESLPCTITDVWISEEKETKETQSADRITIQENEVSEDGVSSTVDQLSD  
910 920 930 940 950 960 960  
920 930 940 950 960 970  
seqid4 IHIEPGTNDSQHSKCDVDKSVQPEPFFHKVVHSEHLNLVPQVQSVQCSPEESFAFRSHSH  
IPI000 IHIEPGTNDSQHSKCDVDKSVQPEPFFHKVVHSEHLNLVPQVQSVQCSPEESFAFRSHSH  
970 980 990 1000 1010 1020  
980 990 1000 1010 1020 1030  
seqid4 LPPKNKNKNSLLIGLSTGLFDANNPKMLRTCSLPDLSKLFRTLMDVPTVGDRVQDNLEID  
IPI000 LPPKNKNKNSLLIGLSTGLFDANNPKMLRTCSLPDLSKLFRTLMDVPTVGDRVQDNLEID  
1030 1040 1050 1060 1060 1070 1080  
1040 1050 1060 1070 1080 1090  
seqid4 EIKDENIKEGPSDSEDIVFEETDTDLQELQASMEQLLREQPGEYSEEESVLKNSDVEP  
IPI000 EIEDENIKEGPSDSEDIVFEETDTDLQELQASMEQLLREQPGEYSEEESVLKNSDVEP  
1090 1100 1110 1120 1130 1140 1140  
1100 1110 1120 1130 1140 1150  
seqid4 TANGTDVADEDNNPSSESALNEEWHSDNSDGEIASECECSVFNHLEELRLHLEQEMGFE  
IPI000 TANGTDVADEDNNPSSESALNEEWHSDNSDGEIASECECSVFNHLEELRLHLEQEMGFE  
1150 1160 1170 1170 1180 1190 1200  
1160 1170 1180 1190 1200 1210  
seqid4 KFFEVYEKAIHEDEDENIEICSKIVQNILGNEHQHLYAKILHLMADGAYQEDNDE  
IPI000 KFFEVYEKAIHEDEDENIEICSKIVQNILGNEHQHLYAKILHLMADGAYQEDNDE  
1210 1220 1230 1240 1250